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Panel Discussion presentation: "An Introduction to the Dryad Repository"

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University of North Carolina at Chapel Hill

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An Introduction to the Dryad Repository

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Dryad is an international repository of data underlying peer-reviewed articles in the basic and applied biosciences.

Dryad enables scientists to validate published findings, explore new analysis methodologies, repurpose data for research questions unanticipated by the original authors, and perform synthetic studies.

Dryad is governed by a consortium of journals that collaboratively promote data archiving and ensure the sustainability of the repository.

<http://datadryad.org>

Brussels Declaration on STM Publishing

“Raw research data should be made freely available to all researchers. Publishers encourage the public posting of the raw data outputs of research. Sets or sub-sets of data that are submitted with a paper to a journal should wherever possible be made freely accessible to other scholars”

Signatories include Elsevier, Nature Publishing Group, Springer, Oxford U Press, Wiley-Blackwell. A total of 46 publishers and 13 trade organizations.

http://www.stmassoc.org/public_affairs_brussels_declaration.php

Defining the need

- ❖ Data no longer published within the article
- ❖ Data is not shared or only shared selectively
- ❖ Data that is not archived is eventually lost
- ❖ Specialized repositories (e.g., GenBank) cover only certain data types and do so incompletely
- ❖ Supplementary materials not the best long term option
- ❖ Funding agencies and journals mandating data archiving

TABLE III^a.*Measurements of Twenty-eight Adult and Young Females which Perished.*

	TOTAL LENGTH.	ALAR EXTENT.	WEIGHT.	LENGTH OF BEAK AND HEAD.	LENGTH OF HUMERUS.	LENGTH OF FEMUR.	LENGTH OF TIBIO- TARSUS.	WIDTH OF SKULL.	LENGTH OF KEEL OF STERNUM.
37 ♀	155	240	26.3	31.4	.709	.710	1.125	.614	.815
38 ♀	156	240	25.8	31.5	.715	.678	1.127	.597	.812
39 ♀	160	242	26.	32.6	.740	.732	1.157	.597	.854
40 ♀	1521	2323	23.23	30.3	.6762	.683	1.048	.590	.780
41 ♀	160	250	26.5	31.7	.741	.731	1.187	.615	.886
42 ♀	155	237	24.2	31.	.727	.723	1.118	.610	.787
43 ♀	157	245	26.9	32.2	.766	.751	1.2272	.620	.841
44 ♀	1653	245	27.7	33.12	.7801	.7573	1.195	.633	.805
45 ♀	1532	2312	23.9	30.1	.6803	.6623	1.0423	.592	.781
46 ♀	162	239	26.1	30.3	.709	.685	1.062	.587	.911
47 ♀	162	243	24.6	31.6	.741	.729	1.162	.605	.840
48 ♀	159	245	23.6	31.8	.727	.700	1.129	.610	.855
49 ♀	159	247	26.	30.9	.711	.666	1.098	.580	.7492
50 ♀	155	243	25.	30.9	.730	.711	1.127	.598	.839
51 ♀	162	252	24.8	31.9	.752	.738	1.180	.615	.875
52 ♀	1521	2301	22.82	30.4	.682	.664	1.0423	.5511	.7341
53 ♀	159	242	24.8	30.8	.717	.667	1.090	.575	.809
54 ♀	155	238	24.6	31.2	.706	.702	1.102	.588	.7583
55 ♀	163	249	30.52	33.41	.767	.7671	1.2073	.6401	.896
56 ♀	163	242	24.8	31.	.713	.713	1.128	.607	.813
57 ♀	156	237	23.9	31.7	.718	.716	1.090	.611	.800
58 ♀	159	238	24.7	31.5	.726	.701	1.145	.600	.800
59 ♀	161	245	26.0	32.1	.751	.704	1.142	.607	.819
60 ♀	155	235	22.61	30.7	.695	.692	1.119	.584	.771
61 ♀	162	247	26.1	31.9	.751	.735	1.157	.618	.802
62 ♀	1534	237	24.8	30.6	.732	.718	1.172	.594	.802
63 ♀	162	245	26.2	32.5	.728	.731	1.102	.614	.832
64 ♀	164	248	26.1	32.3	.730	.707	1.159	.592	.823
Average . .	158	241	25.3	31.4	.726	.709	1.131	.601	.820
General average for 64 birds . . .	160	245	25.8	31.5	.728	.709	1.128	.601	.834

Bumpus HC (1898) The Elimination of the Unfit as Illustrated by the Introduced Sparrow, *Passer domesticus*. A Fourth Contribution to the Study of Variation. pp. 209-226 in *Biological Lectures from the Marine Biological Laboratory*, Woods Hole, Mass.

The gap between attitude and practice

- ❖ Authors in the British Medical Journal randomly received either a *general* or *specific* request to share their data (n=29)
- ❖ Researchers receiving specific requests for data were less likely, and slower, to respond.
- ❖ Only one researcher released data. Others requested further information, clarification, or authorship.

“As soon as results of a study are published, authors have a conflict of interest, and are not well placed to judge the suitability of third-party analyses of the data.”

Reidpath DD, Allotey P (2001) Data sharing in medical research: an empirical investigation. *Bioethics* 15, 125-134

Sharing-on-request is not effective

- ❖ Requested data from from 141 articles in American Psychological Association journals.
- ❖ “6 months later, after ... 400 emails, [sending] detailed descriptions of our study aims, approvals of our ethical committee, signed assurances not to share data with others, and even our full resumes...” only 27% of authors complied

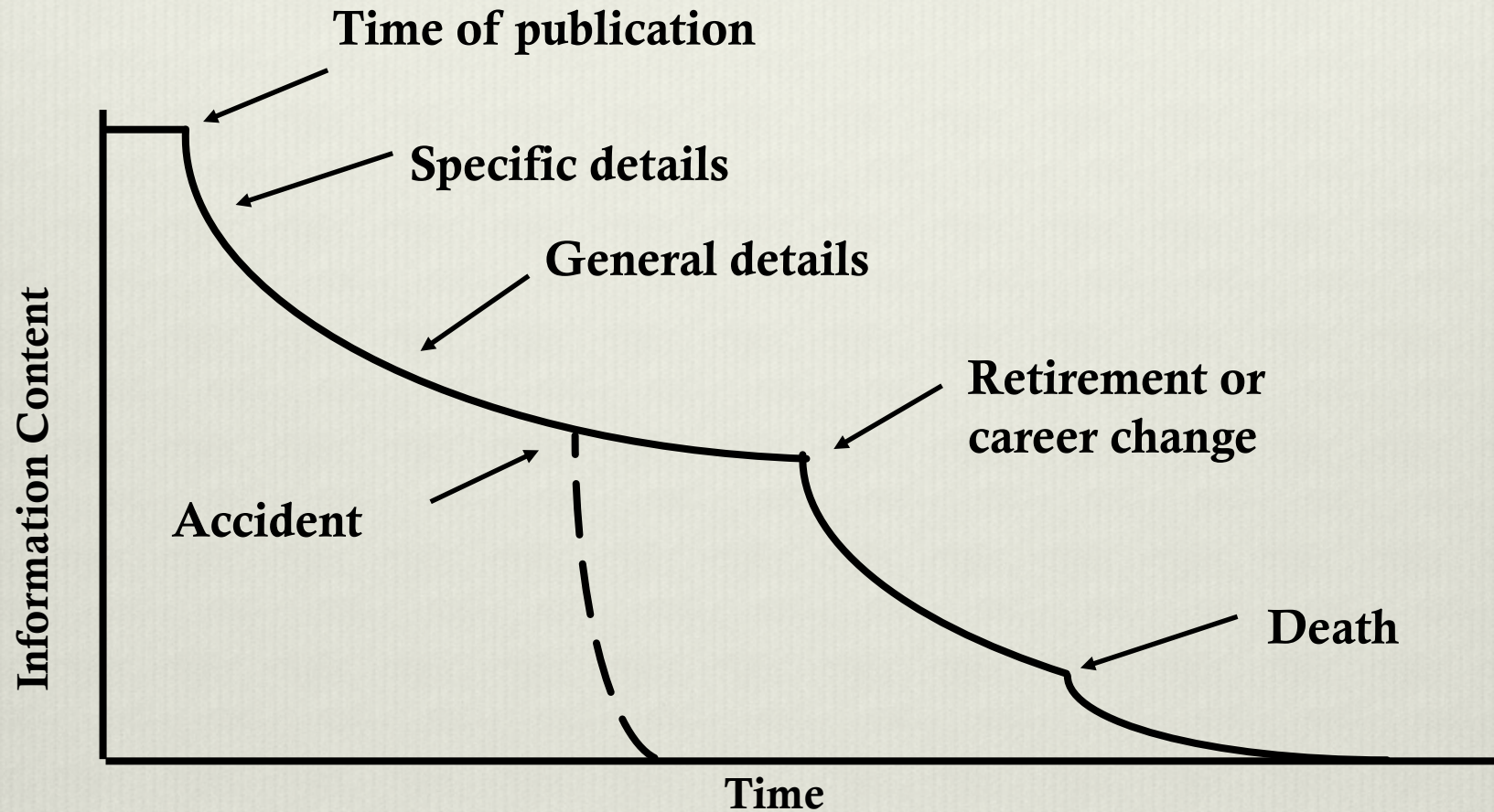
Wicherts, J.M., Borsboom, D., Kats, J., & Molenaar, D. (2006). The poor availability of psychological research data for reanalysis. *American Psychologist*, 61, 726-728.

Why do authors withhold data?

- ❖ In a survey of 1240 geneticists
 - ❖ 47% had been denied at least one request for data or materials in the preceding 3 yrs
 - ❖ 28% reported that they had been unable to confirm published research because of data withholding
- ❖ The most common reasons cited for withholding:
 - ❖ Too much effort to produce the data (80%)
 - ❖ Protecting the ability of a junior colleague to publish (64%)
 - ❖ Protecting their own ability to publish (57%)

Campbell et al. (2002) Data withholding in academic genetics: Results from a national survey. JAMA 287, 473-480.

Data entropy



Michener, W. K., J. W. Brunt, J. Helly, T. B. Kirchner, and S. G. Stafford. 1997. Non-geospatial metadata for the ecological sciences. *Ecological Applications* 7:330-342.

Potential archiving solutions

Author-managed websites

Avoids some of the hazards of informal sharing, but is fragile.

Specialized databases (e.g. GenBank, PDB)

Will cover some datatypes well, some not at all; High quality data, but with greater submission burden; Diversity endangers sustainability

Supplementary materials online

Publisher provides basic infrastructure, but with low level of service.

Public repositories

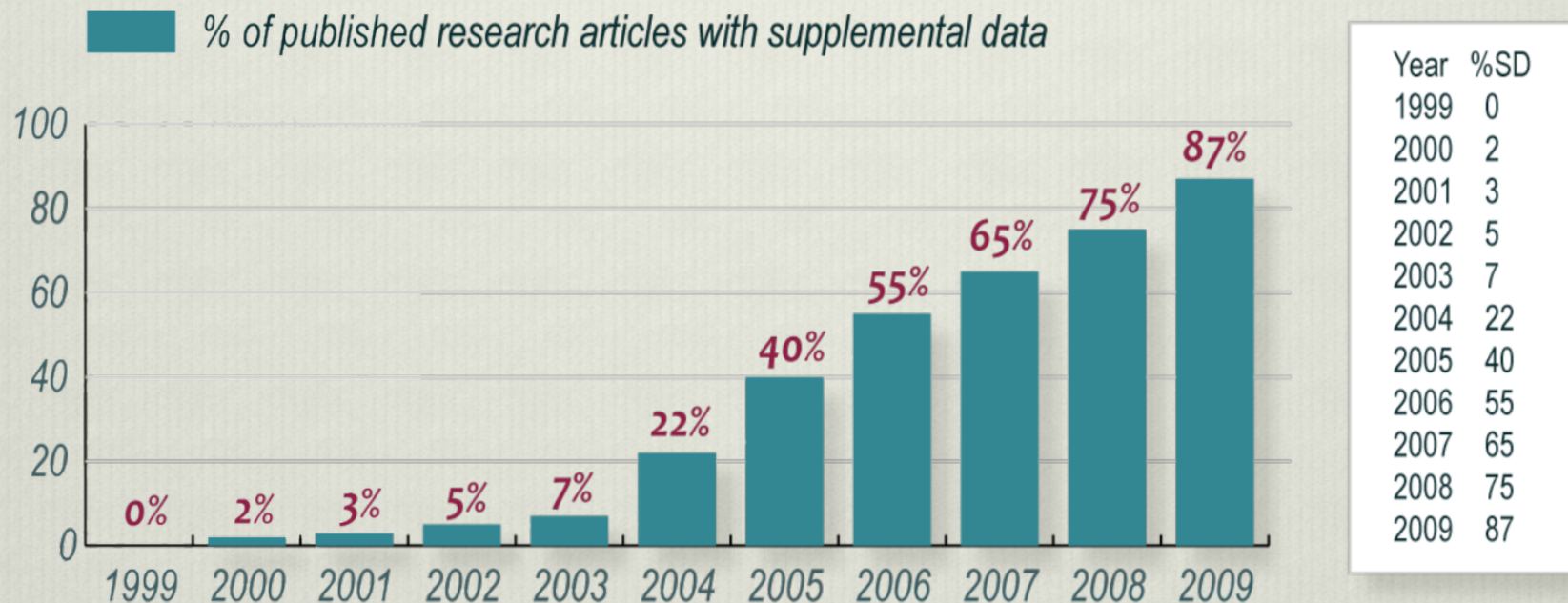
Institutional or disciplinary

About 85% of relevant studies submit DNA sequence data to GenBank

Journal	No. of Studies	Data not submitted to GenBank
Evolution	39	6
MBE	109	4
Nature	42	3
PLoS Biology	30	3
PNAS	30	1
Science	30	2

Noor MAF, Zimmerman KJ, Teeter KC (2006) Data sharing: How much doesn't get submitted to GenBank? PLoS Biol 4(7): e228.

Rapid growth in supplemental data



“Beginning November 1, 2010, The Journal of Neuroscience will no longer allow authors to include supplemental material when they submit new manuscripts and will no longer host supplemental material on its web site for those articles. When articles are published, authors will be allowed to include a footnote with a URL that points to supplemental material on a site they support and maintain, together with a brief description of what the supplemental material includes, but that supplemental material will not be reviewed or hosted by The Journal.”

The Journal of Neuroscience, August 11, 2010, 30(32):10599-10600

NSF Data Management Plans

- ❖ A new requirement for a one page supplement to all proposals
- ❖ To include:
 - ❖ The types of data to be produced
 - ❖ The standards that would be applied for format, metadata content, etc.
 - ❖ Provisions for archiving and preservation
 - ❖ Access policies and provisions
 - ❖ Plans for eventual transition or termination of the data collection after the NSF funding period

Joint Data Archiving Policy

Data are important products of the scientific enterprise, and they should be preserved and usable for decades in the future.

As a condition for publication, data supporting the results in the article should be deposited in an appropriate public archive.

Authors may elect to embargo access to the data for a period up to a year after publication.

Exceptions may be granted at the discretion of the editor, especially for sensitive information.

Whitlock, M. C., M. A. McPeck, M. D. Rausher, L. Rieseberg, and A. J. Moore. 2010. Data Archiving. *American Naturalist*. 175(2):145-146.
doi:10.1086/650340



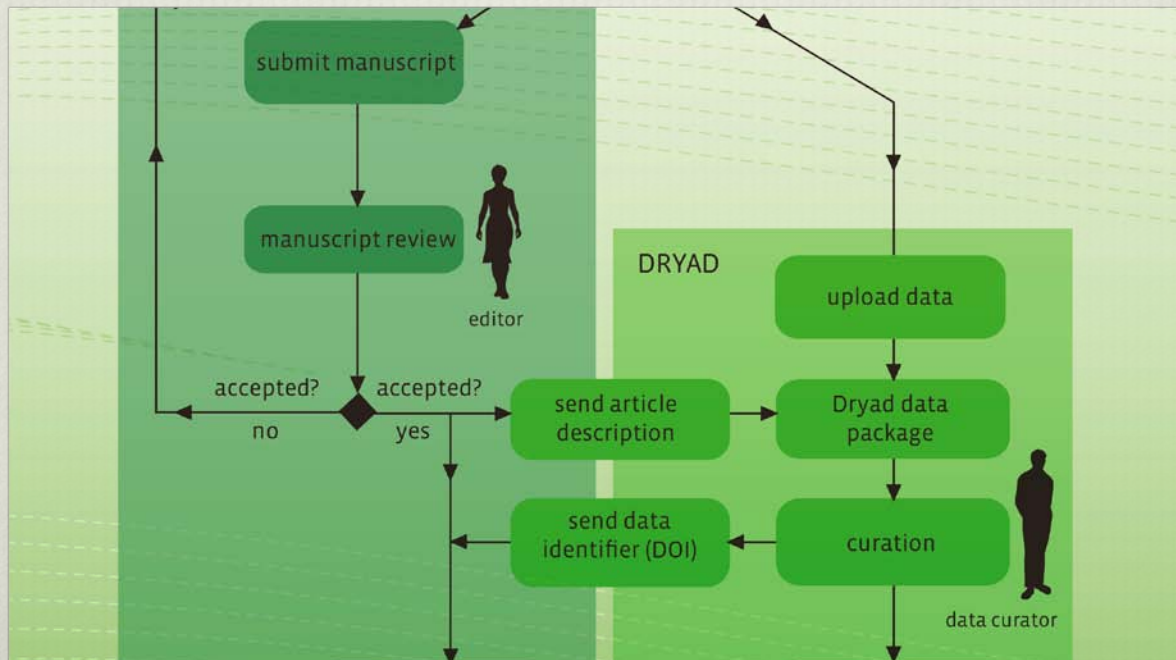
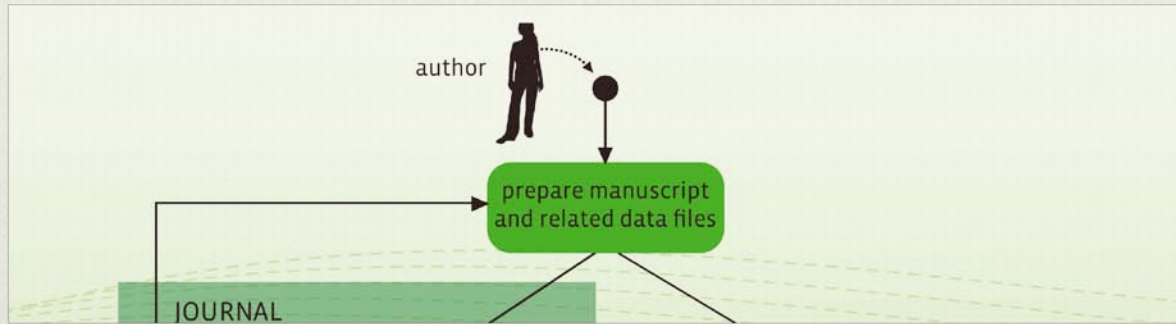
❖ **The End**

- ❖ To make data archiving and reuse a standard function of scholarly communication.

❖ **The Means**

- ❖ Assigning permanent identifiers (DOI) and promoting data citations
- ❖ Publishing data access and download statistics
- ❖ Allowing contents to be updated post-publication
- ❖ Open terms of reuse (Creative Commons Zero), no paywalls
- ❖ Short-term embargoes
- ❖ Searchable across publishers & institutions, by human or machine
- ❖ Metadata are machine harvestable, contents machine-retrievable
- ❖ Preservation services, incl. migration of formats
- ❖ Governed by journals (both publishers and societies)
- ❖ Sustained by the economy of scholarly publishing

An ingest workflow



Example Dryad data package

Data from: Genetic and evolutionary correlates of fine-scale recombination rate variation in *Drosophila persimilis*

When using this data, please cite the original article:

Stevison LS, Noor MAF (2010) Genetic and evolutionary correlates of fine-scale recombination rate variation in *Drosophila persimilis*. *Journal of Molecular Evolution* 71(5-6): 332-345. doi:10.1007/s00239-010-9388-1

Additionally, please cite the Dryad data package:

Stevison LS, Noor MAF (2010) Data from: Genetic and evolutionary correlates of fine-scale recombination rate variation in *Drosophila persimilis*. Dryad Digital Repository. doi:10.5061/dryad.1877

[Cite](#) | [Share](#)

Dryad Package Identifier doi:10.5061/dryad.1877 102 views

Individual Data Files	SNPMarkers.csv	38 views	9 downloads
	Recombinationintervals.csv	38 views	11 downloads
	chromosome2alignmentannotated.gz	43 views	10 downloads
	Perl scripts for analysis	33 views	10 downloads

Abstract Recombination is fundamental to meiosis in many species and generates variation on which natural selection can act, yet fine-scale linkage maps are cumbersome to construct. We generated a fine-scale map of recombination rates across two major chromosomes in *Drosophila persimilis* using 181 SNP markers spanning two of five major chromosome arms. Using this map, we report significant fine-scale heterogeneity of local recombination rates. However, we also observed "recombinational neighborhoods," where adjacent intervals had similar recombination rates after excluding regions near the centromere and telomere. We further found significant positive associations of fine-scale recombination rate with repetitive element abundance and a 13-bp sequence motif known to associate with human recombination rates. We noted strong crossover interference extending 5–7 Mb from the initial crossover event. Further, we observed that fine-scale recombination rates in *D. persimilis* are strongly correlated with those obtained from a comparable study of its sister species, *D. pseudoobscura*. We documented a significant relationship between recombination rates and intron nucleotide sequence diversity within species, but no relationship between recombination rate and intron divergence between species. These results are consistent with selection models (hitchhiking and background selection) rather than mutagenic recombination models for explaining the relationship of recombination with nucleotide diversity within species. Finally, we found significant correlations between recombination rate and GC content, supporting both GC-biased gene conversion (BGC) models and selection-driven codon bias models. Overall, this genome-enabled map of fine-scale recombination rates allowed us to confirm findings of broader-scale studies and identify multiple novel features that merit further investigation.

Scientific Names *Drosophila persimilis*
Drosophila pseudoobscura
Drosophila miranda

Keywords genome evolution
molecular evolution

Date Deposited 2010-08-20T14:58:27Z

Dryad submission system

Fields marked with an asterisk (*) are required. For more information on expected contents for a field, hold your mouse over the field in question.

Publication metadata

Title*:

Data from: Evolution in extreme environments: replicated phenoty

Authors*:

Add

Last name, e.g. Smith

First name + initial, e.g. Donald F.

☐ Tobler, Michael

☐ Palacios, Maura

☐ Chapman, Lauren

☐ Bierbach, David

☐ Plath, Martin

☐ Arias-Rodriguez, Lenin

☐ Garcia De Leon, Francisco

☐ Mateos, Mariana

Remove selected

Journal name*:

Evolution

Abstract:

We investigated replicated ecological speciation in the livebearing fishes *Poecilia mexicana* and *P. sulphuraria* (Poeciliidae), which inhabit freshwater habitats and have also colonized multiple sulfidic springs in southern Mexico. These

DOI:

Journal issue:

Volume

Number

Year

Primary contact for data associated with this article:

Tobler, Michael

Subject keywords:

Add

☐ Ecological speciation

☐ hydrogen sulfide

☐ hypoxia

☐ local adaptation

☐ morphological differentiation

☐ Poecilia

Remove selected

Integrated submission with partner repositories

Data file *

Please upload your data file or provide the identifier of a file located in another repository

☒

☐ External file identifier

Data file description

Title*:

Description:

Repository selection dropdown:

- (please select a repository)
- TreeBASE
- GenBank
- KNB
- OTHER REPOSITORY

Upload data files to partner repositories (optional):

☒ **example_data.txt**

Finalize submission

Finalize submission

When you have added all data files for this publication, press the button below when the descriptions are complete and the files are not corrupted. A confirmation email will be sent to you.

Data DOI in a published article

VOL. 177, NO. 4 THE AMERICAN NATURALIST APRIL 2011

Multiple Benefits Drive Helping Behavior in a Cooperatively Breeding Bird: An Integrated Analysis

Sjouke A. Kingma,^{1,*} Michelle L. Hall,^{1,2,3} and Anne Peters^{1,4}

1. Max Planck Institute for Ornithology, Vogelwarte Radolfzell, Schlossallee 2, 78315 Radolfzell, Germany; 2. Mornington Wildlife Sanctuary, Australian Wildlife Conservancy, PMB 925, Derby, Western Australia 6728, Australia; 3. Research School of Biology, Australian National University, Canberra, Australian Capital Territory 0200, Australia; 4. School of Biological Sciences, Monash University, Clayton, Victoria 3800, Australia

Submitted July 23, 2010; Accepted January 3, 2011; Electronically published March 10, 2011

Dryad data: <http://dx.doi.org/10.5061/dryad.8210>.

Another example

Significant genetic boundaries and spatial dynamics of giant pandas occupying fragmented habitat across southwest China

LIFENG ZHU¹, SHANNING ZHANG²,
XIAODONG GU³, FUWEN WEI¹

Article first published online: 21 JAN 2011

DOI: 10.1111/j.1365-294X.2011.04999.x

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Issue



Molecular Ecology

Volume 20, Issue 6, pages
1122–1132, March 2011

Nature Reserve and Wawushan Nature Reserve for help during fieldwork. We thank Dr Wang Shichang for assistance with data analysis.

Data accessibility

Jump to...

Data deposited at Dryad: doi:10.5061/dryad.8035.

References

Jump to...

Bandelt HJ, Forster P, Rohlf A (1999) Median-joining networks for inferring intraspecific phylogenies. *Molecular Biology and Evolution*, **16**, 37–48.

Another example, in PLoS ONE

RESEARCH ARTICLE



Stalking the Fourth Domain in Metagenomic Data: Searching for, Discovering, and Interpreting Novel, Deep Branches in Marker Gene Phylogenetic Trees

[Article](#)[Metrics](#)[Related Content](#)[Comments: 13](#)

Dongying Wu¹, Martin Wu^{1,4}, Aaron Halpern^{2,3}, Douglas B. Rusch^{2,3}, Shibu Yooseph^{2,3}, Marvin Frazier^{2,3}, J. Craig Venter^{2,3}, Jonathan A. Eisen^{1*}

1 Department of Evolution and Ecology, Department of Medical Microbiology and Immunology, University of California Davis Genome Center, University of California Davis, Davis, California, United States of America, **2** The J. Craig Venter Institute,

To add a note, highlight some text. [Hide notes](#)

[Make a general comment](#)

Jump to

[Abstract](#)

Data and protocol availability

We've made the following data and protocols available for the public: (1) GOS and reference sequences for RecA and RpoB; (2) Subfamilies of RecA and RpoB ([Table 1,3](#)); (3) Alignments and Newick format phylogenetic trees of RecA and RpoB ([Figure 1,3](#)); (4) Sequences of the genes that share assemblies with the novel *recAs*. ([Table 2](#)); (5) GOS ss-rRNA sequence reads; (6) the Lek clustering program. The data and protocols are available at http://bobcat.genomecenter.ucdavis.edu/GOSrecA_DATA/index.html. The data have also been submitted to the Dryad repository <http://datadryad.org/> - <http://dx.doi.org/10.5061/dryad.8384>.

Searching and browsing

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in order descending

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Dryad (22)

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Hegarty MJ, Batstone T, Barker GL, Edwards KJ, Abbott RJ, Hiscock SJ (2010) Data from: Nonadditive changes to cytosine methylation as a consequence of hybridization and genome duplication in *Senecio* (Asteraceae). *Molecular Ecology* doi:10.5061/dryad.7851

Paun O, Bateman RM, Fay MF, Hedrén M, Civeyrel L, Chase MW (2010) Data from: Stable epigenetic effects impact adaptation in allopolyploid orchids (*Dactylorhiza*: Orchidaceae). *Molecular Biology and Evolution* doi:10.5061/dryad.1521

Thiel-Egenter C, Holderegger R, Brodbeck S, Gugerli F (2009) Data from: Concordant genetic breaks, identified by combining clustering and tessellation methods, in two co-distributed alpine plant species. *Molecular Ecology* doi:10.5061/dryad.1343

Maley J, Winker K (2010) Data from: Diversification at high latitudes: speciation of buntings in the genus *Plectrophenax* inferred from mitochondrial and nuclear markers. *Molecular Ecology* doi:10.5061/dryad.1142

Mikheyev AS, Vo T, Wee B, Singer MC, Parmesan C (2010) Data from: Rapid microsatellite isolation from a butterfly by de novo transcriptome sequencing: performance and a comparison with AFLP-derived distances. *PLoS ONE* doi:10.5061/dryad.1540

Dryad metadata

- ❖ Emphasis on simplicity and interoperability
- ❖ Using Dublin Core plus some additions from PRISM, Darwin Core, and BIBO (planned)
- ❖ Exchanging metadata with DataCite, TreeBASE, others
- ❖ Working toward making metadata available as RDF and publishing a complete application profile using Singapore Framework guidelines

Is Dryad meeting its goals?

- ❖ Are people using the data?
- ❖ Does it improve the efficiency of science?
- ❖ Does it improve the quality of science?
- ❖ Does it expand the capacity of science?

Lessons from the Gene Expression Omnibus

OPEN ACCESS Freely available online

PLOS one

Sharing Detailed Research Data Is Associated with Increased Citation Rate

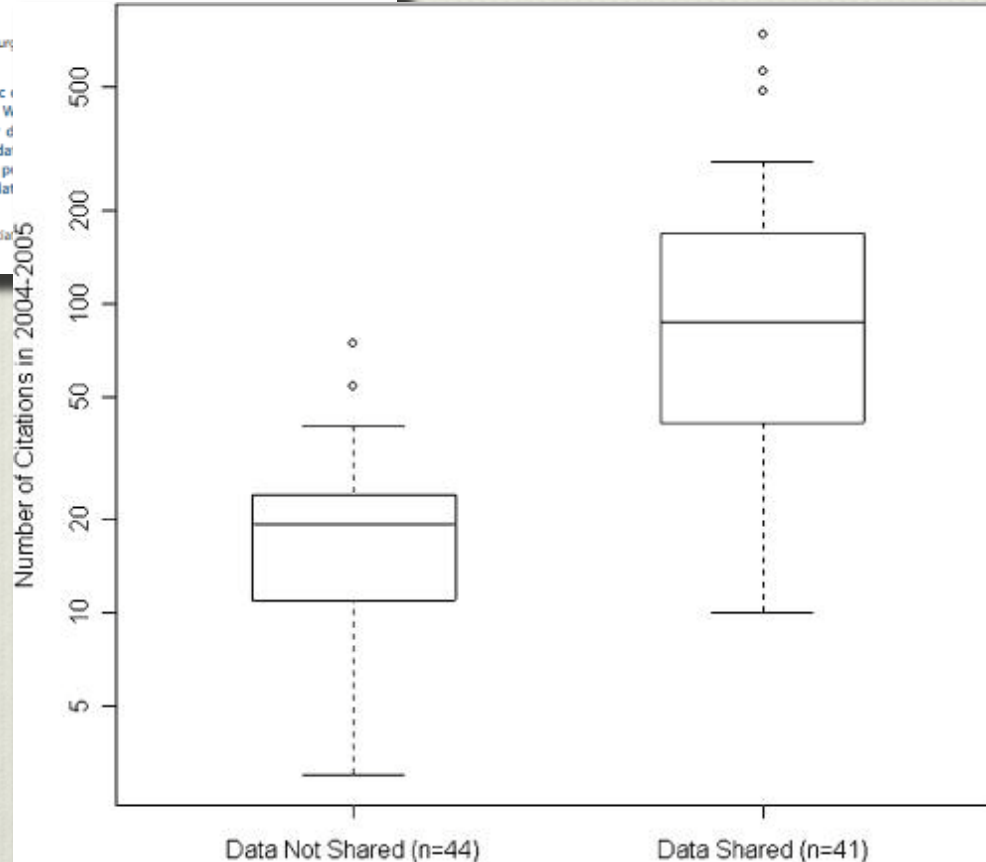
Heather A. Piwowar*, Roger S. Day, Douglas B. Fridsma

Department of Biomedical Informatics, University of Pittsburgh School of Medicine, Pittsburgh

Background. Sharing research data provides benefit to the general scientific community. **Principal Findings.** A microarray clinical trial publications with respect to the availability of their data received 85% of the aggregate citations. Publicly available data received a 69% increase in citations, independently of journal impact factor, date of publication, and author country of origin. **Significance.** This correlation between publicly available data and citations motivate investigators to share their detailed research data.

Citation: Piwowar HA, Day RS, Fridsma DB (2007) Sharing Detailed Research Data Is Associated with Increased Citation Rate. PLoS ONE 2(3): e308. doi:10.1371/journal.pone.0000308

Citations were 69% greater for publications that shared microarray data (right) versus those that did not (left), independent of journal impact factor, date of publication, and author country of origin.



Heather
Piwowar

Piwowar H, et al. (2007) Sharing Detailed Research Data Is Associated with Increased Citation Rate. PLoS ONE 2(3): e308.

Challenges and next steps for Dryad

- ❖ New submission workflows, collaborating with journals to fit into their publication process
- ❖ Handshaking with additional partner repositories
- ❖ Building tools for more efficient curation
- ❖ Linked data / semantic web
- ❖ Name authority control – ORCID, other researcher IDs
- ❖ Subject metadata and controlled vocabularies – HIVE, another MRC project

Disciplinary vs. institutional repositories

- ❖ The infrastructure for data archiving is playing catch-up with the needs of scientists.
- ❖ There is a healthy competition between institutional and disciplinary repositories to meet these needs.
- ❖ The ingest bottleneck will drive the solution
 - ❖ Disciplinary repositories like Dryad can ingest the long tail of orphan published data.
 - ❖ Institutional libraries are best placed to develop the vast array of pre- and post-publication services that data-driven science will require.

Some of the contributors to Dryad

Dryad Consortium Board, journal partners, and data authors

NESCent: Kevin Clarke, Hilmar Lapp, Heather Piwowar, Peggy Schaeffer, Ryan Scherle, Todd Vision

UNC-CH <Metadata Research Center>: Sarah Carrier, Elena Feinstein, Jane Greenberg, Hollie White

Duke: Cliff Cunningham, Mohamed Noor, Kathleen Smith, Marcy Uyenoyama

U British Columbia: Michael Whitlock

NCSU Digital Libraries: Kristin Antelman

Yale/TreeBASE: Youjun Guo, Bill Piel

UNM/LTER/DataONE: Bill Michener, Mark Servilla

Oxford University: David Shotton

British Library: Lee-Ann Coleman, Adam Farquhar



Some Partner Journals

American Society of Naturalists

American Naturalist

Ecological Society of America

Ecology, Ecological Letters, Ecological Monographs, etc.

European Society for Evolutionary Biology

Journal of Evolutionary Biology

Society for Integrative and Comparative Biology

Integrative and Comparative Biology

Society for Molecular Biology and Evolution

Molecular Biology and Evolution

Society for the Study of Evolution

Evolution

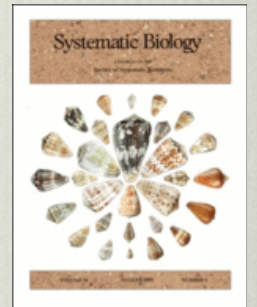
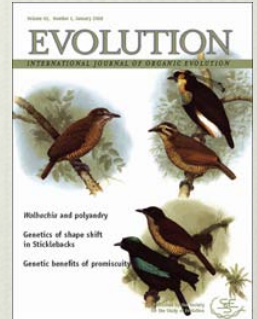
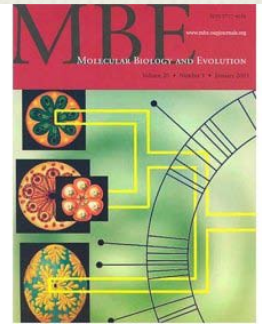
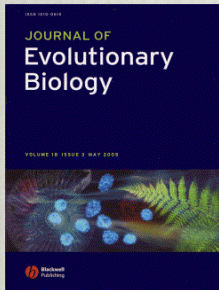
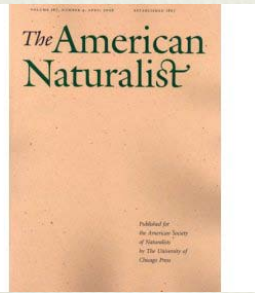
Society for Systematic Biology

Systematic Biology

Commercial journals

Molecular Ecology

Molecular Phylogenetics and Evolution



Initial Funding

- ❖ National Science Foundation (USA)
- ❖ Institute of Museum and Library Services (USA)
- ❖ Joint Information Systems Committee (UK)



Dryad Technology

- ❖ DataONE member node
- ❖ DSpace repository software (open source)
- ❖ Assigning DOIs via California Digital Library
- ❖ Integration with specialized repositories and databases
 - ❖ Federated searching with TreeBASE and KNB LTER
 - ❖ TreeBASE submission (using BagIt and OAI-PMH)
 - ❖ GenBank (planned for future)



<http://datadryad.org>

<http://blog.datadryad.org>

<http://datadryad.org/wiki>

<http://code.google.com/p/dryad>

Facebook & Twitter (#datadryad)